



## SEQUENCE LISTING

<110> Lust, John A.  
<110> Donovan, Kathleen A.

<120> USE OF GENETICALLY ENGINEERED ANTIBODIES TO CD38 TO TREAT MULTIPLE MYELOMA

<130> 150.188US2

<140> 09/730,374

<141> 2000-12-05

<150> PCT/US99/12512

<151> 1999-06-04

<150> 60/088,277

<151> 1998-08-05

<160> 5

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 750

<212> DNA

<213> Artificial Sequence

<220>

<223> A nucleotide sequence encoding a single chain  
variable region fragment (scFv)

<400> 1

ggcccagccg	gccatggcca	agggtccagct	gcaggagtca	ggacctagcc	tagtgcagcc	60
ctcacagcgc	ctgtccataa	cctgcacagt	ctctggttc	tcattaatta	gttatgggtgt	120
acactgggtt	cgccagtctc	caggaaaggg	tctggagtgg	ctgggagtga	tatggagagg	180
tggaagcaca	gactacaatg	cagctttcat	gtccagactg	agcatcacca	aggacaactc	240
caagagccaa	gttttcttta	aatgaacag	tctgcaagct	gatgacactg	ccatataactt	300
ctgtgccaaa	accttgatta	cgacgggcta	tgctatggac	tactggggcc	aagggaccac	360
gtcaccgtc	tcctcaggtg	gaggcgggtc	aggcggaggt	ggctctggcg	gtggcggatc	420
gjacatcgag	ctcactcagt	ctccatcctc	ctttctgtt	tctctaggag	acagagtac	480
cattacttgc	aaggcaagtg	aggacatata	taatcggtt	gcctggatc	agcagaaacc	540
aggaaatgct	cctaggctct	taatatctgg	tgcaaccagt	ttggaaactg	gggttccttc	600
aagattcagt	ggcagtggat	ctggaaagga	ttacactctc	agcattacca	gtcttcagac	660
tgaagatgtt	gtctacttatt	actgtcaaca	gtattggagt	actcctacgt	tcggtgagg	720
gaccaagctg	gaaatcaaac	gggcggccgc				750

<210> 2

<211> 241

<212> PRT

<213> Artificial Sequence

<220>

<223> A polypeptide encoded by an open reading frame of  
SEQ ID NO:1

<400> 2

Gly	Pro	Ala	Gly	His	Gly	Gln	Gly	Pro	Ala	Ala	Gly	Val	Arg	Thr	Pro
1				5				10					15		
Ser	Ala	Ala	Leu	Thr	Ala	Pro	Val	His	Asn	Leu	His	Ser	Leu	Trp	Phe
	20				25				30						
Leu	Ile	Asn	Leu	Trp	Cys	Thr	Leu	Gly	Ser	Pro	Val	Ser	Arg	Lys	Gly
	35				40				45						

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TECH CENTER 1600/2900

Ser Gly Val Ala Gly Ser Asp Met Glu Arg Trp Lys His Arg Leu Gln  
50 55 60  
Cys Ser Phe His Val Gln Thr Glu His His Gln Gly Gln Leu Gln Glu  
65 70 75 80  
Pro Ser Phe Leu Asn Glu Gln Ser Ala Ser His Cys His Ile Leu Leu  
85 90 95  
Cys Gln Asn Leu Asp Tyr Asp Gly Leu Cys Tyr Gly Leu Leu Gly Pro  
100 105 110  
Arg Asp His Gly His Arg Leu Leu Arg Trp Arg Arg Phe Arg Arg Arg  
115 120 125  
Trp Leu Trp Arg Trp Arg Ile Gly His Arg Ala His Ser Val Ser Ile  
130 135 140  
Leu Leu Phe Cys Ile Ser Arg Arg Gln Ser His His Tyr Leu Gln Gly  
145 150 155 160  
Lys Gly His Ile Ser Val Ser Leu Val Ser Ala Glu Thr Arg Lys Cys  
165 170 175  
Ser Ala Leu Asn Ile Trp Cys Asn Gln Phe Gly Asn Trp Gly Ser Phe  
180 185 190  
Lys Ile Gln Trp Gln Trp Ile Trp Lys Gly Leu His Ser Gln His Tyr  
195 200 205  
Gln Ser Ser Asp Arg Cys Cys Tyr Leu Leu Leu Ser Thr Val Leu Glu  
210 215 220  
Tyr Ser Tyr Val Arg Trp Arg Asp Gln Ala Gly Asn Gln Thr Gly Gly  
225 230 235 240  
Arg

<210> 3  
<211> 249  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> A polypeptide encoded by an open reading frame of  
SEQ ID NO:1

<400> 3  
Ala Gln Pro Ala Met Ala Lys Val Gln Leu Gln Glu Ser Gly Pro Ser  
1 5 10 15  
Leu Val Gln Pro Ser Gln Arg Leu Ser Ile Thr Cys Thr Val Ser Gly  
20 25 30  
Phe Ser Leu Ile Ser Tyr Gly Val His Trp Val Arg Gln Ser Pro Gly  
35 40 45  
Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Arg Gly Gly Ser Thr Asp  
50 55 60  
Tyr Asn Ala Ala Phe Met Ser Arg Leu Ser Ile Thr Lys Asp Asn Ser  
65 70 75 80  
Lys Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Ala Asp Asp Thr  
85 90 95  
Ala Ile Tyr Phe Cys Ala Lys Thr Leu Ile Thr Thr Gly Tyr Ala Met  
100 105 110  
Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly  
115 120 125  
Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Asp Ile Glu Leu  
130 135 140  
Thr Gln Ser Pro Ser Ser Phe Ser Val Ser Leu Gly Asp Arg Val Thr  
145 150 155 160  
Ile Thr Cys Lys Ala Ser Glu Asp Ile Tyr Asn Arg Leu Ala Trp Tyr  
165 170 175  
Gln Gln Lys Pro Gly Asn Ala Pro Arg Leu Leu Ile Ser Gly Ala Thr  
180 185 190

Ser Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly  
195 200 205  
Lys Asp Tyr Thr Leu Ser Ile Thr Ser Leu Gln Thr Glu Asp Val Ala  
210 215 220  
Thr Tyr Tyr Cys Gln Gln Tyr Trp Ser Thr Pro Thr Phe Gly Gly Gly  
225 230 235 240  
Thr Lys Leu Glu Ile Lys Arg Ala Ala  
245

<210> 4  
<211> 239  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> A polypeptide encoded by an open reading frame of  
SEQ ID NO:1

<400> 4  
Pro Ser Arg Pro Trp Pro Arg Ser Ser Cys Arg Ser Gln Asp Leu Ala  
1 5 10 15  
Cys Ser Pro His Ser Ala Cys Pro Pro Ala Gln Ser Leu Val Ser His  
20 25 30  
Leu Val Met Val Tyr Thr Gly Phe Ala Ser Leu Gln Glu Arg Val Trp  
35 40 45  
Ser Gly Trp Glu Tyr Gly Glu Val Glu Ala Gln Thr Thr Met Gln Leu  
50 55 60  
Ser Cys Pro Asp Ala Ser Pro Arg Thr Thr Pro Arg Ala Lys Phe Ser  
65 70 75 80  
Leu Lys Thr Val Cys Lys Leu Met Thr Leu Pro Tyr Thr Ser Val Pro  
85 90 95  
Lys Pro Leu Arg Arg Ala Met Leu Trp Thr Thr Gly Ala Lys Gly Pro  
100 105 110  
Arg Ser Pro Ser Pro Gln Val Glu Ala Val Gln Ala Glu Val Ala Leu  
115 120 125  
Ala Val Ala Asp Arg Thr Ser Ser Ser Leu Ser Leu His Pro Pro Phe  
130 135 140  
Leu Tyr Leu Glu Thr Glu Ser Pro Leu Leu Ala Arg Gln Val Arg Thr  
145 150 155 160  
Tyr Ile Ile Gly Pro Gly Ile Ser Arg Asn Gln Glu Met Leu Leu Gly  
165 170 175  
Ser Tyr Leu Val Gln Pro Val Trp Lys Leu Gly Phe Leu Gln Asp Ser  
180 185 190  
Val Ala Val Asp Leu Glu Arg Ile Thr Leu Ser Ala Leu Pro Val Phe  
195 200 205  
Arg Leu Lys Met Leu Leu Leu Ile Thr Val Asn Ser Ile Gly Val Leu  
210 215 220  
Leu Arg Ser Val Glu Gly Pro Ser Trp Lys Ser Asn Gly Arg Pro  
225 230 235

<210> 5  
<211> 750  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> A nucleotide sequence complementary to SEQ ID NO:1  
(presented in 5'-3' orientation)

<400> 5  
gcggccgccc gtttatttc cagcttggtc cctccaccga acgttaggagt actccaatac

tgttgacagt	aataaggtagc	aacatcttca	gtctgaagac	tggtaatgct	gagagtgtaa	120
tcctttccag	atccactgcc	actgaatctt	gaaggaaccc	cagttccaa	actgggtgc	180
ccagatatta	agagcctagg	agcatttctt	ggtttctgct	gataccaggc	taaccgatta	240
tatatgtct	cacttgcctt	gcaagtaatg	tgactctgt	ctcctagaga	tacagaaaag	300
gaggatggag	actgagttag	ctcgatgtcc	gatccgcccac	cgccagagcc	acctccgcct	360
gaaccgcctc	cacctgagga	gacggtgacc	gtggtccctt	ggccccagta	gtccatagca	420
tagcccgtcg	taatcaaggt	tttggcacag	aagtatatgg	cagtgtcatc	agcttgcgaga	480
ctgttcattt	taaagaaaaac	ttggctcttg	gagttgtcct	tggtgatgct	cagtctggac	540
atgaaagctg	cattgttagtc	tgtgcttcca	cctctccata	tcactcccag	ccactccaga	600
ccctttcccg	gagactggcg	aacccagtgt	acaccataac	taattaatga	gaaaccagag	660
actgtgcagg	ttatggacag	gcgctgtgag	ggctgcacta	ggctaggtcc	tgactcctgc	720
agctggacct	tggccatggc	cggctgggccc				750